

	Regulatory Domain	
CtCtcC	-MSIEHILIDDDPHILALLSEILGARNFSVSSAPGVKQAIKQISNCPFDLIISDMNMPD	59
SmDetD	MSAAPSVFLIDDDRLRKAMQQTLEAGFTVSSFASATEALAEADSFAGIVISDIRMPG	60
StNtrC	-MQRGIVWVDDSSIRWVLERALAGAGLTCTTFENGNEVLAALASKTPDVLSDIRMPG	59
PaNtrC	MSRSETVWIVDDRSIRWVLEKALQEGMTTVSFDASDVIGRLGQQPDVLIISDIRMPG	60
EcAtoC	MTAINRILIVDDENVRRLSTAFALQGFETHCANNRGTALHLFADIHPDVLMDIRMPG	60
	: : * * : : . : . : . : . : : : * : . *	
CtCtcC	GSGLDIQYTKQHRPQTPILVITAFGTIONAVEAMRFGAFNYLTKPFSPDALFTLIAKAE	119
SmDetD	MDGLALFGKVLADPDLPMLVTGHGDIPIHMAVQAIQDGAYDFIAKPPAADRLVQSARRAE	120
StNtrC	MDGLALLKQTKQRHPLPVIIIMTAHSDLDAAVSAIYQGAFDYLPKPPDIDEAVALVERAI	119
PaNtrC	ASGLDLAQIRELHPLPVIIIMTAHSDLDAAVSAIYQGAFDYLPKPPDIDEAVALVERAI	120
EcAtoC	MDGIKALKEMRSHETRTPVILMTAYAEVETAVEALRCGAFDYVIKPPDDELNLIVQAL	120
	. * : : : * : : * : : * : : * : : * : : *	
CtCtcC	ELQALQDNLFQSQG--SSISHPLIAESPSMKQLLDKARRAANSSANIFVHGSGCGKE	177
SmDetD	EKRRLVMENRSLRRAEAASEGLPLIGQTPAMERLRQTLKHIADTDVDVLVAGETGSGKE	180
StNtrC	SHYQEQQPRNIEVNGP---TDMIGEAPAMQDLFRIIIGRLSRSSISVLINGESGTGKE	175
PaNtrC	QHAQEQQGLELPANQAR---TPEIIGEAPAMQEVFRAIGRLSHSNITVLINGESGTGKE	176
EcAtoC	QLQSMKKESRHLHQAALSTSWQGHILTNFAMMDICKDTAKIALSQASVLISGESGTGKE	180
	. : : * : : : : : : : : : * : * : *	
	ATPase Domain	
CtCtcC	NLSFFIHKHSPRSTKPYIKVNCAIPDTLLESEFFGHHKGAFTGAATKKVGRFELAHQGT	237
SmDetD	VVATLLHQWSRRRTGNFVALNCGALPETVIESELFGHHPGAFTGAATKKRIGRIEHASGGT	240
StNtrC	LVAHALHRHSPRAKAPFIALNMAAIPKDLIESELFGHHPGAFTGAATIRQGRFEQADGGT	235
PaNtrC	LVAHALHRHSPRAKAPFIALNMAAIPKDLMESELFGHHPGAFTGAATAQRGRFEQADGGT	236
EcAtoC	LIARAIHYNRSRAKGPFIKVNCAALPESLSELFGHHPGAFTGAATLRQGLFERANEGT	240
	. : * * : : : * . : : * : * : * : * : * : * : *	
CtCtcC	LLDEITEPIHLOAKLLRAIQEQEFHIGGIKTLPVNIRFLATSNRDLLEAEITKVLRO	297
SmDetD	LFLDEIEAMPAPATQVKMLRVLEAREITPLGTNLTRPVDIRVVAAKVDLGDPAARGDFRE	300
StNtrC	LFLDEIGDMPADVTQRLRLVLDAGQFYRVGGYAPVKVDVRIIAATHONLERRVDEGKFRE	295
PaNtrC	LFLDEIGDMPADVTQRLRLVLDAGQFYRVGGYTPVKVDVRIIAATHONLESVRDQKFRE	296
EcAtoC	LLDEIGEMPLVLQAKLLRILQEREFEFIRGGHQTIKVDIRIIAATNRDLQAMVKEGTFRE	300
	* : * * : * : * : * : : : : * : * : * : * : *	
CtCtcC	DLYRLSVISLHPIPLDRKEDILPLAHYLEKFCMNNKPPKTLSELAQRNLLDYSWPG	357
SmDetD	DLYRLNVVTLSSIPLRERRDIPLLFSHFLARASERFGEVPAISAMRAYLATHSWPG	360
StNtrC	DLFHLNVIRIHLPPLRERRDIPRLARHFLQVAARELGVEAKLLHPETETALTRLAWPG	355
PaNtrC	DLFHLNVIRIHLPRLADRREDIPALRHFLSRAAQELAVEPKLLKAETEYELKNLWPG	356
EcAtoC	DLFYRLNVHILIPPLRDRREDISLLANHFLQKFSSENQRDIIDIPMAMSLTAWSPG	360
	* : * * . : : * : * : * : * : * : * : * : * : *	
CtCtcC	NVRELSNVLERTVILENDPAITPSMLALL-----	386
SmDetD	NVRELSHFAERVALGVEGNLGVPA-----AP	387
StNtrC	NVRLQNTCRLWTVMAAGQEVLIQDLPGELFEASTPDSPSHLPPDSWATLLAQWADRRLR	415
PaNtrC	NVRLQNTCRLWTVMAAGREHVIDDLPELLETOPO----DSAPANWEQALRWADQALG	412
EcAtoC	NIRELSNVIERAVMNSGPIIFSEDLPQIRQPCVNAGEVK-----TAP	404
	* : * : . : . :	
	DNA Binding Domain	
CtCtcC	-----	386
SmDetD	ASSGATLPERLERYEADILKQALTAHCGDVKETLQVLGIPRKTFFYDKLQRHGINRADYVE	447
StNtrC	SGHQNLSEAQPELERTLLTALRHTQGHKQEAARLLGWGRNTLTRKLELGME-----	469
PaNtrC	RGQSNLLDSAVPAPERIMETALKHTAGRRRDAVLLGWGRNTLTRKIKELGMNVGDADD	472
EcAtoC	VGERNL-KEIKRVEKRIIMEVLEQQEGNRTALMLGISRRALMYKLQEQYGDIPADV--	461
CtCtcC	-----	386
SmDetD	RAGFGRPNAISK	460
StNtrC	-----	469
PaNtrC	EGDD-----	476
EcAtoC	-----	461

Figure S1. Clustal W sequence alignment of CtcC from *Chlamydia trachomatis* (Ct) with other σ^{54} -regulatory proteins from *Sinorhizobium meliloti* (Sm), *Salmonella Typhimurium* (St), *Pseudomonas aeruginosa* (Pa), and *Escherichia coli* (Ec) shows that the overall domain structure is conserved among bacterial species. The residues involved in σ^{54} interaction are highly conserved (red box), as is the E242 residue (red arrow) responsible for polarization of the ATP molecule allowing for hydrolysis and the D54 residue that is phosphorylated by the sensor kinase protein.